

Structure and composition of exfoliation aggregates

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INTRODUCTION

Exfoliation syndrome (XFS) is a condition characterized by the production of insoluble fibrillar aggregates (exfoliation material; XFM) in the eye and elsewhere. Many patients with XFS progress to exfoliation glaucoma (XFG), a significant cause of global blindness. We used quantitative mass spectrometry to analyze the composition of XFM in lens capsule specimens and in aqueous humor (AH) samples from patients with XFS, patients with XFG, and unaffected individuals.

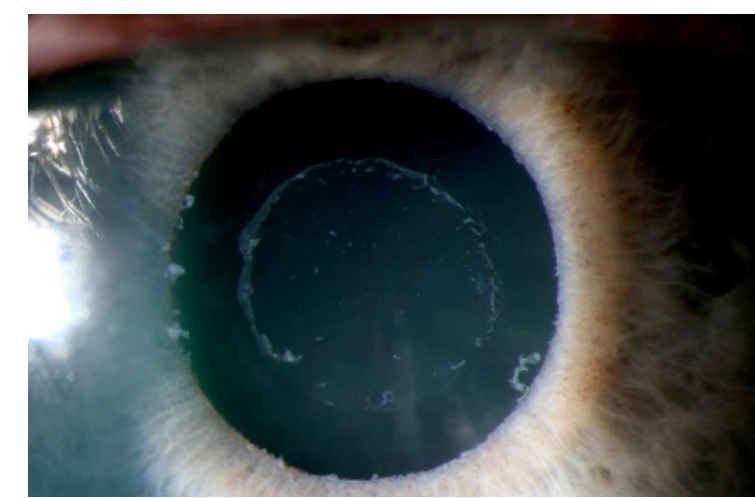


Figure 1. Dust-like aggregates accumulate on the anterior surface of the lens in a patient with exfoliation syndrome

DESIGN & METHODS

Pieces of lens capsule and samples of AH were obtained with consent from patients undergoing cataract surgery. Tryptic digests of capsule or AH were analyzed by high-performance liquid chromatography–mass spectrometry and relative differences between samples were quantified using the tandem mass tag technique. The distribution of XFM on the capsular surface was visualized by SEM and super-resolution light microscopy.

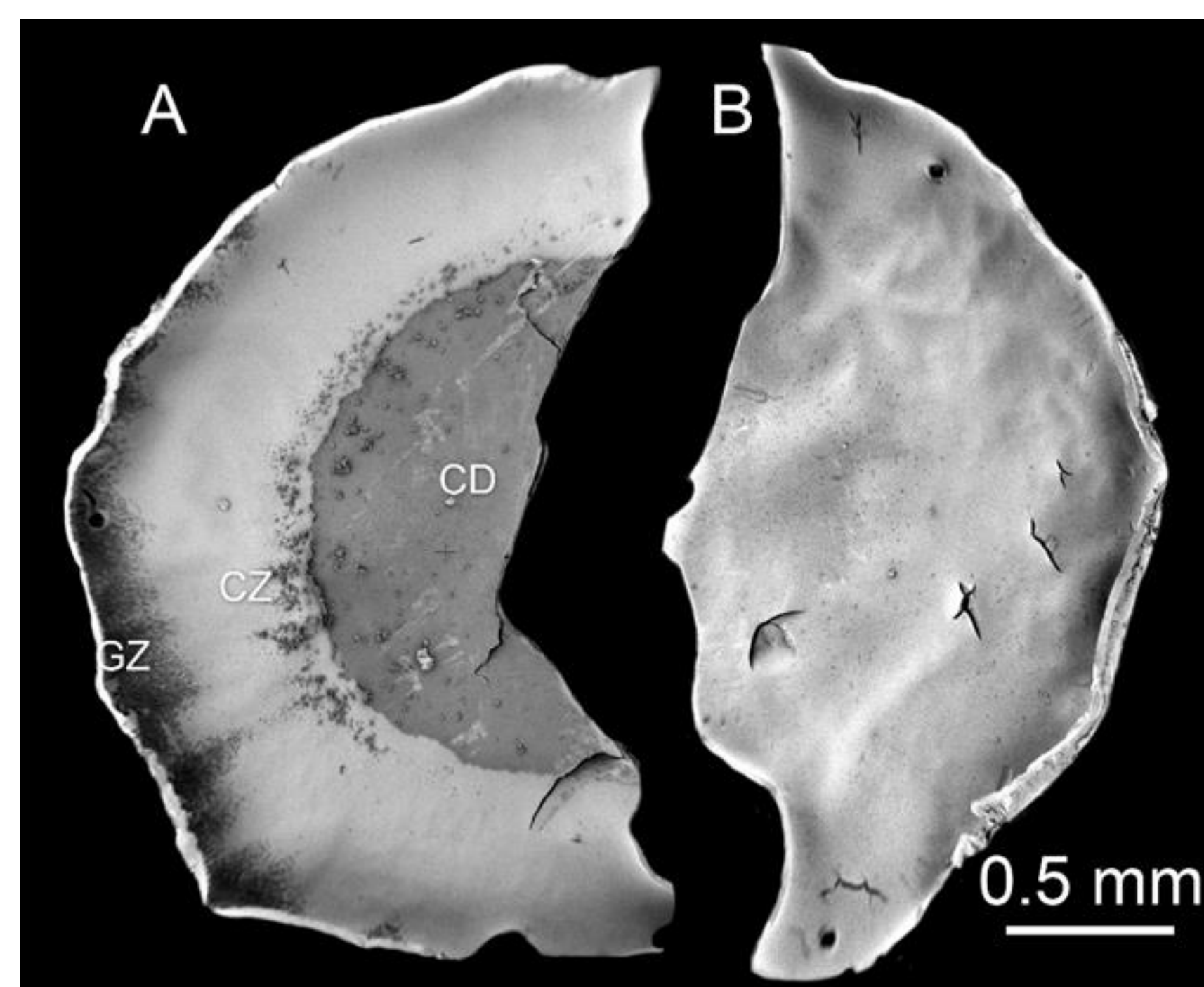


Figure 2. Scanning electron micrograph showing the presence of exfoliation material on a capsular specimen from an XFS patient (A) or a control sample (B, from a patient without XFS). Comparative proteomic analysis was used to identify proteins present in XFS samples and absent in controls. CD, central disk; CZ, clear zone; GZ, granular zone.

DIAGRAM OR EXAMPLE

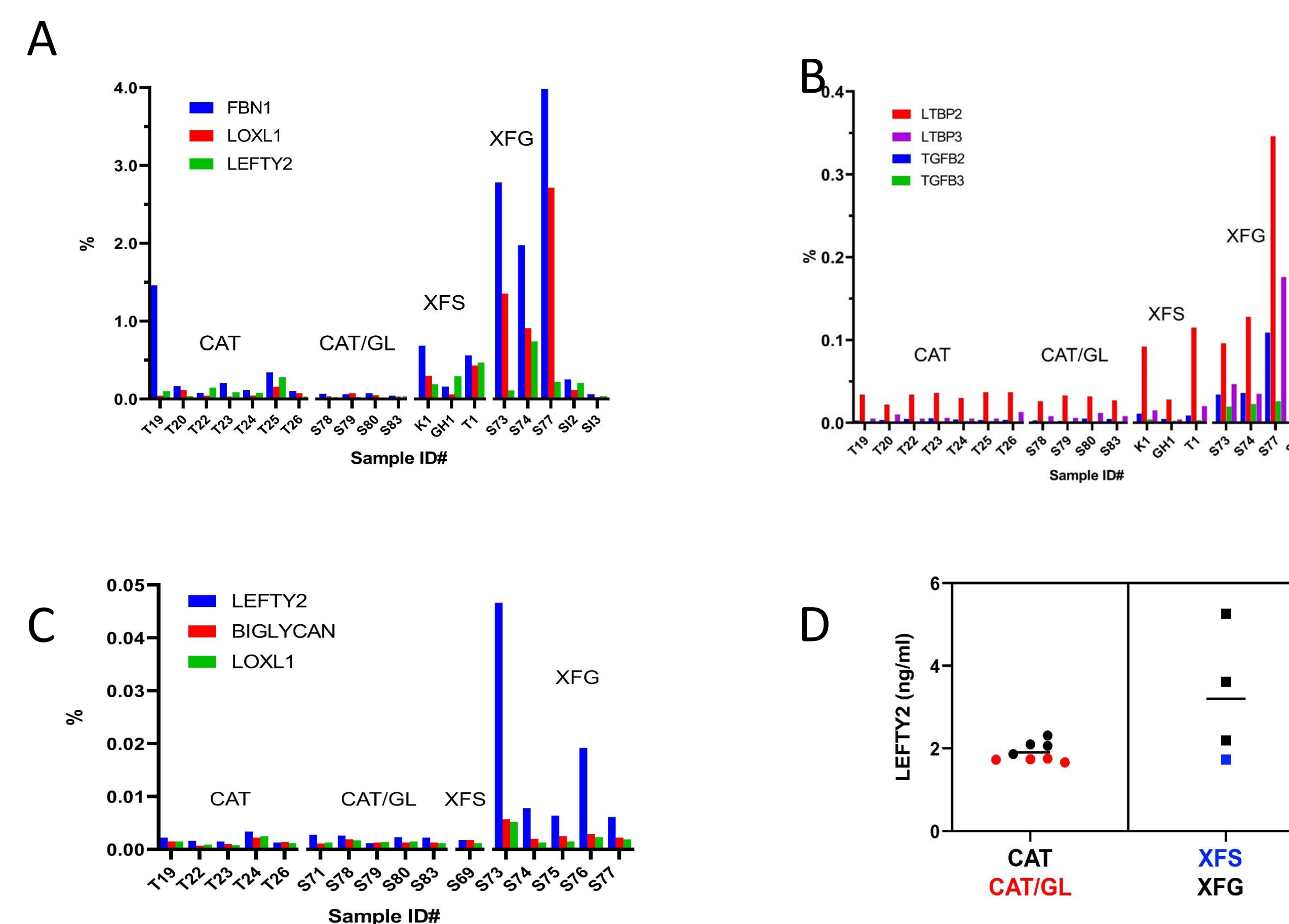
Sample ID	Age	Sex	Diagnosis	Visual Acuity	IOP	Glaucoma	Protein 1	Protein 2	Protein 3	Protein 4	Protein 5	Protein 6	Protein 7	Protein 8	Protein 9	Protein 10	Protein 11	Protein 12	Protein 13	Protein 14	Protein 15	Protein 16	Protein 17	Protein 18	Protein 19	Protein 20	Protein 21	Protein 22	Protein 23	Protein 24	Protein 25	Protein 26	Protein 27	Protein 28	Protein 29	Protein 30	Protein 31	Protein 32	Protein 33	Protein 34	Protein 35	Protein 36	Protein 37	Protein 38	Protein 39	Protein 40	Protein 41	Protein 42	Protein 43	Protein 44	Protein 45	Protein 46	Protein 47	Protein 48	Protein 49	Protein 50	Protein 51	Protein 52	Protein 53	Protein 54	Protein 55	Protein 56	Protein 57	Protein 58	Protein 59	Protein 60	Protein 61	Protein 62	Protein 63	Protein 64	Protein 65	Protein 66	Protein 67	Protein 68	Protein 69	Protein 70	Protein 71	Protein 72	Protein 73	Protein 74	Protein 75	Protein 76	Protein 77	Protein 78	Protein 79	Protein 80	Protein 81	Protein 82	Protein 83	Protein 84	Protein 85	Protein 86	Protein 87	Protein 88	Protein 89	Protein 90	Protein 91	Protein 92	Protein 93	Protein 94	Protein 95	Protein 96	Protein 97	Protein 98	Protein 99	Protein 100
T19	65	M	XFS	20/40	16	Yes	1.5	2.5	3.5	4.5	5.5	6.5	7.5	8.5	9.5	10.5	11.5	12.5	13.5	14.5	15.5	16.5	17.5	18.5	19.5	20.5	21.5	22.5	23.5	24.5	25.5	26.5	27.5	28.5	29.5	30.5	31.5	32.5	33.5	34.5	35.5	36.5	37.5	38.5	39.5	40.5	41.5	42.5	43.5	44.5	45.5	46.5	47.5	48.5	49.5	50.5	51.5	52.5	53.5	54.5	55.5	56.5	57.5	58.5	59.5	60.5	61.5	62.5	63.5	64.5	65.5	66.5	67.5	68.5	69.5	70.5	71.5	72.5	73.5	74.5	75.5	76.5	77.5	78.5	79.5	80.5	81.5	82.5	83.5	84.5	85.5	86.5	87.5	88.5	89.5	90.5	91.5	92.5	93.5	94.5	95.5	96.5	97.5	98.5	99.5	100.5

Table 1. Patient demographics and clinical details

Uniprot accession/protein ID	Total change	p-value	corrected p-value	XFS and XFG (Avg. Intensity)	CONTROL (Avg. Intensity)	confidence
EXPT 1 (XFS and XFG vs CAT)						
Q8B977/LOXL1	18.69	4.39E-08	2.21E-05	4.82E+06	2.47E+05	high
O00292/LFY2	4.59	1.54E-06	3.88E-04	3.14E+06	7.17E+05	high
P10800/TGFB3	7.61	6.03E-06	9.80E-04	9.21E+04	1.21E+04	high
Q29291/FBN1	4.06	1.48E-05	1.80E-03	2.55E+05	6.20E+04	high
P25182/TGFB2	5.99	4.90E-05	4.32E-03	1.58E+05	2.68E+04	high
P25087/COR2A2	2.74	3.38E-04	2.43E-02	4.62E+04	1.68E+04	med
Q9N615/LTBP3	4.43	3.99E-04	2.53E-02	1.54E+05	3.47E+04	med
P35001/MFAP2	3.33	4.72E-04	2.64E-02	4.38E+05	1.32E+05	med
Q14767/LTBP2	3.89	6.11E-04	3.98E-02	6.29E+05	2.38E+05	med
EXPT 2 (XFS and XFG vs CAT/GU)						
Q8H4Y0/CRPPL	18.74	2.61E-09	1.47E-06	6.33E+04	3.38E+03	high
P10800/TGFB3	13.74	1.95E-07	5.41E-05	3.17E+04	2.31E+03	high
P35553/FBN1	18.15	6.67E-07	1.50E-04	4.75E+06	2.94E+05	high
O00292/LFY2	7.65	4.21E-06	4.7E-04	9.82E+05	1.28E+05	high
Q8B977/LOXL1	13.82	1.50E-05	1.06E-03	3.19E+06	2.31E+05	high
Q14767/LTBP2	3.42	3.80E-05	2.08E-03	4.87E+05	1.42E+05	high
Q9N615/LTBP3	3.73	3.71E-04	6.72E-03	1.53E+05	4.10E+04	high
P25182/TGFB2	4.05	4.28E-04	7.58E-03	7.13E+04	1.80E+04	high

Table 2. Differentially expressed proteins in XFS and XFG samples vs. controls.

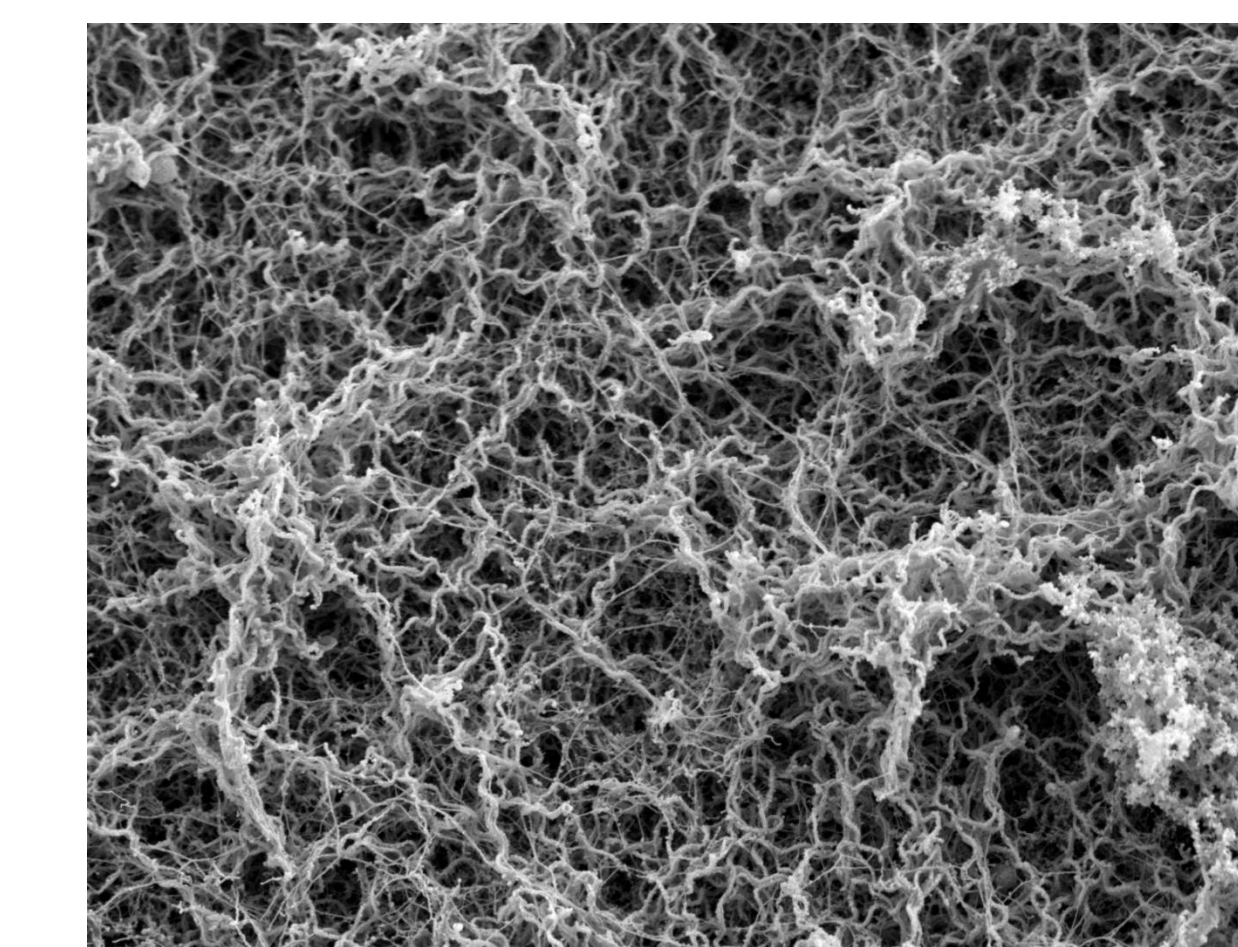
RESULTS



Differentially expressed proteins in individual patient samples (T19, T20, etc.). A. XFS aggregates are characterized by strong expression of fibrillin 1 (FBN1), Lysyl oxidase-like 1 (LOXL1), and left-right differentiation factor-2 (LEFTY2). B. Aggregates also contain elevated levels of TGFbeta and latent-TGFbeta binding proteins (LTBP's). C. In aqueous humor samples LOXL1 is not elevated but biglycan and, especially, LEFTY2, are increased. D. ELISA analysis showing that LEFTY levels are elevated in samples from XFG patients. CAT, cataract; CAT/GL, cataract with glaucoma; XFS exfoliation syndrome patient, XFS; and XFG, exfoliation glaucoma.

CONCLUSIONS

This quantitative study provides new insights into the composition of pseudoexfoliation aggregates. Three proteins (FBN1, LOXL1 and LEFTY2) were especially abundant in the aggregates, although other members of the TGFbeta signaling pathway (TGFbeta2, TGFbeta3, LTBP2 (Latent TGFbeta binding protein 2) LTBP3) were also prominent.



Scanning electron microscopy detected two types of fibers in the XFM aggregates: thin (10 nm) straight fibers and thick (30 nm) rough surfaced, helical fibers.

NEXT STEPS

This project provided information on the ultrastructure and composition of pseudoexfoliation aggregates. Moving forward, we would like to localize the proteins identified by mass spec analysis on the fibrils that comprise the material. Specifically, we hope to understand the ultrastructural relationship between fibrillin-1 and LOXL1.

LEFTY2, a novel member of the TGFbeta growth factor family, was identified in both the capsule and aqueous humor samples from pseudoexfoliation patients. The level of LEFTY2 was particularly elevated in samples from pseudoexfoliation patients who had developed glaucoma. Based on this observation, we are currently organizing a larger study to determine whether LEFTY2 can serve as a biomarker for glaucoma progression. We are also interested in determining the cellular source of LEFTY2 and exploring its potential role in disease progression.

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